




Bacterial Whole Genome Sequencing Report


October 12, 2023

Sample ID: SRR21152630

Sequencing Technology

Nextera XT DNA Library Preparation
MiSeq 2 x 250 Read Generation

Sequence Statistics		Quality Scale
		Low  High
Filename	SRR21152630-R1.fastq.gz	SRR21152630-R2.fastq.gz
File size	128.4 MB	133.7 MB
Mean Read Score	32.96	32.55
Q30 Passing	94.1%	91.3%
Sequence Depth	250.6X	Calculated by number of reads x 240/Genome Length
Genome Length	5,000,000bp	Based on MLST identification

Assembly Statistics				Quality Scale			
				Low			High
Scaffolds	Total length	Longest scaffold	Scaffolds >1K nt	Genome >1K nt	N50	L50	
200	4,709,882	648,908	31	99.51	399,180	5	

De novo assembly performed using SPAdes v3.13.0 .

Multi Locus Sequence Typing (MLST)

Organism ID: **Salmonella enterica** Schema-Sequence type: **senterica_achtman_2-46**

MLST Detail: aroC(10) dnaN(7) hemD(21) hisD(12) purE(15) sucA(12) thrA(12)

Data obtained using 2.23.0. Software website: <https://github.com/tseemann/mlst>

Information on MLST schemes and allelic profiles can be found at pubMLST.org

Serotyping for Salmonella Isolates

Predicted serotype(s) **Newport**
Predicted antigenic profile **8:e,h:1,2**
Predicted subspecies **Salmonella enterica subspecies enterica (subspecies I)**

Note:

Data obtained using SeqSero. Software website: <https://github.com/denglab/SeqSero2>

Antimicrobial Resistance Analysis

Results were obtained using [AMRFinder](#). AMRFinder uses BLASTX to search a hierarchy of gene families with predetermined cutoffs.

AMRFinder

No Antimicrobial Resistance Genes found.

AMRFinder

Revision 3.11.2

<https://github.com/ncbi/amr/wiki>

Definitions were taken from the AMRFinder documentation.

Target Identifier- This is from the FASTA define for the DNA sequence

Contig id- Contig name

Start- 1-based coordinate of first nucleotide coding from protein in DNA sequence on contig

Stop- 1-based coordinate of last nucleotide coding for protein in DNA sequence on contig

Gene symbol- Gene or gene-family symbol for protein hit

Protein name- Full-text name for the protein

Method- Type of hit found by AMRFinder one of five options

ALLELE- 100% sequence match over 100% of length to a protein named at the allele level in the AMRFinder database

EXACT- 100% sequence match over 100% of length to a protein in the database that is not a named allele

BLAST- BLAST alignment is >90% of length and >90% identity to a protein in a the AMRFinder database

PARTIAL- BLAST alignment is >50% of length, but <90% of length and >90% identity

HMM- HMM was hit above the cutoff, but there was not a BLAST hit that met standards for BLAST or PARTIAL

Target length- The length of the query protein. The length of the BLAST hit for translated-DNA searches

Reference protein length- The length of the AMR Protein in the database (NA if HMM-only hit)

Scope- The AMRFinderPlus database is split into core AMR proteins that are expected to have an effect on resistance and plus proteins of interest added with less stringent inclusion criteria. These may or may not be expected to have an effect on phenotype

Element subtype- Further elaboration of functional category into *ANTIGEN*, *BIOCIDE*, *HEAT*, *METAL*, *PORIN* if more specific category is available, otherwise the element is repeated

% Coverage of reference protein- % covered by blast hit (NA if HMM-only hit)

% Identity to reference protein- % amino-acid identity to reference protein (NA if HMM-only hit)

Alignment length- Length of BLAST alignment in amino acids (NA if HMM-only hit)

Accession of closest protein- RefSeq accession for protein hit by BLAST (NA if HMM-only hit)

Name of closest protein- Full name assigned to the AMRFinder database protein (NA if HMM-only hit)

HMM id- Accession for the HMM

HMM description- The family name associated with the HMM